

Application No.: 08881509

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: SEE ENCLOSED NOTE

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Schwadron

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1644 RUSH
7/11/99

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/881,509B

DATE: 09/10/1999
TIME: 09:50:19

INPUT SET: S33262.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: SCHENDEL, Dolores J.
6
7 (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA
8
9 (iii) NUMBER OF SEQUENCES: 44
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
13 (B) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
14 (C) CITY: Washington
15 (D) STATE: DC
16 (E) COUNTRY: USA
17 (F) ZIP: 20005-5701
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 08/881,509
27 (B) FILING DATE: June 24, 1997
28 (C) CLASSIFICATION:
29
30 (viii) ATTORNEY/AGENT INFORMATION:
31 (A) NAME: Kitts, Monica Chin
32 (B) REGISTRATION NUMBER: 36,105
33 (C) REFERENCE/DOCKET NUMBER: 564-7015
34
35 (ix) TELECOMMUNICATION INFORMATION:
36 (A) TELEPHONE: (202) 638-5000
37 (B) TELEFAX: (202) 638-4810
38
39
40 (2) INFORMATION FOR SEQ ID NO: 1:
41
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 1341 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: both
46 (D) TOPOLOGY: linear

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48      (ix) FEATURE:
49          (A) NAME/KEY: CDS
50          (B) LOCATION:1..801
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52      (ix) FEATURE:
53          (A) NAME/KEY: sig_peptide
54          (B) LOCATION:1..54
55
56      (ix) FEATURE:
57          (A) NAME/KEY: mat_peptide
58          (B) LOCATION:55..801
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60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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64      -18          -15          -10          -5
65
66      AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA      96
67      Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
68          1          5          10
69
70      CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT      144
71      Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
72      15          20          25          30
73
74      TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT      192
75      Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
76          35          40          45
77
78      ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT      240
79      Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
80          50          55          60
81
82      ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC      288
83      Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
84          65          70          75
85
86      CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG      336
87      Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
88          80          85          90
89
90      CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC      384
91      Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
92          95          100          105          110
93
94      CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT      432
95      Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
96          115          120          125
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98      GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG      480
99      Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val

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100	130	135	140	
101				
102	TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA			528
103	Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu			
104	145	150	155	
105				
106	GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC			576
107	Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser			
108	160	165	170	
109				
110	AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT			624
111	Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile			
112	175	180	185	190
113				
114	CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG			672
115	Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys			
116	195	200	205	
117				
118	CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC			720
119	Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn			
120	210	215	220	
121				
122	CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT			768
123	Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe			
124	225	230	235	
125				
126	AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA			821
127	Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser			
128	240	245		
129				
130	GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG			881
131				
132	AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCGGCA			941
133				
134	ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA			1001
135				
136	CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA			1061
137				
138	GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC			1121
139				
140	CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCTGGAG			1181
141				
142	AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTCATA AAGAAATACA TAGTATTCTT			1241
143				
144	CTTCTCAAGA CGTGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG			1301
145				
146	GGCGTGTGTG ATGTCCTGCT GCCGATGCCT TCATTAAAAT			1341
147				
148				
149	(2) INFORMATION FOR SEQ ID NO: 2:			
150				
151	(i) SEQUENCE CHARACTERISTICS:			
152	(A) LENGTH: 267 amino acids			

RAW SEQUENCE LISTING PATENT APPLICATION *US/08/881,509B*

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153         (B) TYPE: amino acid
154         (D) TOPOLOGY: linear
155
156         (ii) MOLECULE TYPE: protein
157
158         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
159
160 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
161 -18          -15          -10          -5
162
163 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
164          1          5          10
165
166 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
167 15          20          25          30
168
169 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
170          35          40          45
171
172 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
173          50          55          60
174
175 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
176          65          70          75
177
178 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
179          80          85          90
180
181 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
182 95          100          105          110
183
184 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
185          115          120          125
186
187 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
188          130          135          140
189
190 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
191          145          150          155
192
193 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
194          160          165          170
195
196 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
197          175          180          185          190
198
199 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
200          195          200          205
201
202 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
203          210          215          220
204
205 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe

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206          225          230          235
207
208 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
209      240          245
210
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212 (2) INFORMATION FOR SEQ ID NO: 3:
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214 (i) SEQUENCE CHARACTERISTICS:
215      (A) LENGTH: 936 base pairs
216      (B) TYPE: nucleic acid
217      (C) STRANDEDNESS: both
218      (D) TOPOLOGY: linear
219
220 (ix) FEATURE:
221      (A) NAME/KEY: CDS
222      (B) LOCATION:1..933
223
224 (ix) FEATURE:
225      (A) NAME/KEY: sig_peptide
226      (B) LOCATION:1..63
227
228 (ix) FEATURE:
229      (A) NAME/KEY: mat_peptide
230      (B) LOCATION:64..933
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232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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234 ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA      48
235 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
236 -21 -20          -15          -10
237
238 GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA      96
239 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
240 -5          1          5          10
241
242 CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC      144
243 Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
244 15          20          25.
245
246 TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT      192
247 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
248 30          35          40
249
250 CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC      240
251 Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
252 45          50          55
253
254 GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG      288
255 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
256 60          65          70          75
257
258 AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC      336

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SEQUENCE VERIFICATION REPORT
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